

0590

1015

#2

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/940,101

DATE: 09/18/2001

TIME: 10:06:56

Input Set : A:\GENENT.072A2.txt

Output Set: N:\CRF3\09182001\I940101.raw

4 <110> APPLICANT: Gerritsen, Mary
 5 Sliwkowski, Mark X.
 7 <120> TITLE OF INVENTION: ErbB4 ANTAGONISTS
 10 <130> FILE REFERENCE: GENENT.072A2
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/940,101
 C--> 12 <141> CURRENT FILING DATE: 2001-08-27
 12 <150> PRIOR APPLICATION NUMBER: 60/229,679
 13 <151> PRIOR FILING DATE: 2000-09-01
 15 <150> PRIOR APPLICATION NUMBER: 60/265,516
 16 <151> PRIOR FILING DATE: 2001-01-31
 18 <160> NUMBER OF SEQ ID NOS: 4
 20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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 23 <211> LENGTH: 5484
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Homo sapiens
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 29 tgggtgagcc ttctcggtgc ggcggggacc gtccagccca gcgattctca gtcagtgtgt 120
 30 gcaggaacgg agaataaaact gagctctctc tctgacacctgg aacagcagta ccgagccctg 180
 31 cgcaagtact atgaaaactg tgaggttgc atgggcaacc tggagataac cagcattgag 240
 32 cacaaccggg acctctccctt cctgcggctc gtgcgagaag tcacaggctc cgtgttagtg 300
 33 gctcttaatc agtttcgtta cctgcctctg gagaatttac gcattattcg tggacaaaa 360
 34 ctttatgagg atcgatatgc cttggcaata tttttaaact acagaaaaga tggaaacttt 420
 35 ggacttcaag aacttggatt aaagaacttgc acagaaaatcc taaatggtgg agtctatgt 480
 36 gaccagaaca aattcccttg ttatgcagac accattcatt ggcagatat tggtcgaaac 540
 37 ccatggcctt ccaacttgcac tcttgcgtca acaaattgtt gttcaggatg tggacgttgc 600
 38 cataagtccct gtactggccg ttgctggggc cccacagaaa atcattgcca gactttgaca 660
 39 aggacgggtgt gtgcagaaca atgtgacggc agatgtacg gaccttacgt cagtgactgc 720
 40 tgccatcgag aatgtgctgg aggctgctca ggacctaagg acacagactg cttgcctgc 780
 41 atgaatttca atgacagtgg agcatgtgtt actcagtgtc cccaaacctt tgtctacaat 840
 42 ccaaccaccc ttcaacttgc gcacaatttc aatgcääagt acacatatgg agcattctgt 900
 43 gtcaagaaat gtccacataa ctttgcgtt gattccagtt cttgtgtgcg tgcctggccct 960
 44 agttccaaga tggaaatgtt agaaaatggg attaaaatgt taaaaccttgc cactgacatt 1020
 45 tgcccaaaag cttgtgtatgg cattggcaca ggatcattga tgtcagctca gactgtggat 1080
 46 tccagtaaca ttgacaaaatt cataaaactgt accaagatca atgggaattt gatctttcta 1140
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 48 aacgtctttc ggacagtgcg agagataaca ggtttcctga acatacagtc atggccacca 1260
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 51 ctgaaggaaa tcagcgccagg aaacatctat attactgaca acagcaacct gtgttattat 1440
 52 cataccatta actggacaac actcttcagc acaatcaacc agagaatagt aatccgggac 1500
 53 aacagaaaag ctgaaaattt tactgctgaa ggaatgggtgt gcaaccatct gtgtccagt 1560
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 55 aggtatctgca tagagtcttg taacctctat gatggtgaat ttcgggagtt tgagaatggc 1680
 56 tccatctgtg tggagtgta cccccagtgt gagaagatgg aagatggcct cctcacatgc 1740
 57 catggaccgg gtcctgacaa ctgtacaaag tgctctcatt taaaagatgg cccaaactgt 1800

ENTERED

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58 gtggaaaaat gtccagatgg cttacagggg gcaaacagtt tcatttcaa gtatgctgat 1860
 59 ccagatcggg agtgcaccc atgcacca aactgcaccc aagggtgtaa cggtcccact 1920
 60 agtcatgact gcatttacta cccatggacg ggccattcca ctttaccaca acatgctaga 1980
 61 actccctga ttgcagctgg agtaattggt gggcttca ttctggcat tgtgggtctg 2040
 62 acatttctg tttatgttag aaggaaagagc atcaaaaaga aaagagcctt gagaagattc 2100
 63 ttggaaacag agttggtgg a cccatggca cagcacccaa tcaagctcaa 2160
 64 cttcgatattt tgaaagaaac tgagctgaag aggtaaaag tccttggctc aggtgcttt 2220
 65 ggaacggttt ataaaggtat ttgggtaccc gaaggagaaa ctgtgaagat tcctgtggct 2280
 66 attaagattc ttaatgagac aactggtccc aaggcaaatg tggagttcat ggtgaagct 2340
 67 ctgatcatgg caagtatgg a tcatccacac ctatccgggt tgctgggtgt gtgtctgagc 2400
 68 ccaaccatcc agctggttac tcaactttag cccatggct gcctgttggaa gtatgtccac 2460
 69 gaggcacaagg ataacattgg atcacaactg ctgcttaact ggtgtgtccaa gatagctaa 2520
 70 ggaatgatgt acctggaaaga aagacgactc gttcatcggg atttggcagc ccgtaatgtc 2580
 71 ttagtgaat ctccaaacca tggaaaatc acagattttg ggctagccag actcttggaa 2640
 72 ggagatgaaa aagagttacaa tgctgtatgg gggaaagatgc caattaaatg gatggctctg 2700
 73 gagtgatatac attacaggaa attcaccat cagagtgacg tttggagcta tggagttact 2760
 74 atatggaaac ttagtgcaccc ttggaggaaaa ccctatgtatgg gaaattccaa gcgagaaatc 2820
 75 cctgattttat tagagaaagg agaacgtttt cctcagccctc ccatctgcac tattgacgat 2880
 76 tacatggtca ttggcaatgg tttggatgatt gatgtgaca gtagaccaa atttaaggaa 2940
 77 ctggctgctg agtttcaag gatggctcg a cccatccaa gatacctagt tattcagggt 3000
 78 gatgatcgta tgaagcttcc cagtcaccaat gacagcaatg tctttcagaa tctcttggat 3060
 79 gaagaggatt tggaaagatat gatggatgatc gaggagttact tggccctca ggcttcaac 3120
 80 atccccaccc ccatctatac ttccagagca agaattgact cgaataggag tggaaattgg 3180
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 83 gaagctctg tggcacaggg tgctactgtt gggatggatc atgactctg ctgtaatggc 3360
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 87 cttttgttt ctggagaaaa aaatggagac cttcaagcat tggataatcc cgaatatcac 3600
 88 aatgcatcca atggccacc caaggccgag gatgagttatg tgaatgagcc actgtaccc 3660
 89 aacacccctt ccaacacccctt gggaaaagct gatgtacccatg agaacaacat actgtcaatg 3720
 90 ccagagaagg ccaagaaagc gtttgaccaac cctgactact ggaaccacag cctgccaccc 3780
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 93 ctgaagccag gcactgtgtt gccgcctccaa ctttacagac accggaaatac tgtgggtt 3960
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 102 ataacatccc ttttttttttgcacccatcc 4500
 103 ctttttttttgcacccatcc 4560
 104 ttttttttttgcacccatcc 4620
 105 ctttttttttgcacccatcc 4680
 106 atgatgtgtgc atatttagca tccctggaaa tcataataaa gtttccatggaaacaaaaga 4740

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107 ggccactact ttaagtatac aatctttaaa ataagaaaagg gaggctaata ttttcatgc 4800
108 tatcaaatta tcttcaccct catcctttac attttcaac atttttttt ctccataaat 4860
109 gacactactt gataggccgt tgggtgtctg aagagtagaa gggaaactaa gagacagttc 4920
110 tctgtggttc aggaaaacta ctgatactt caggggtggc ccaatgaggg aatccattga 4980
111 actggaagaa acacactgga ttgggtatgt ctaccctggca gatactcaga aatgttagttt 5040
112 gcaacttaagc tgtaattttt tttgttctt ttctgaactc cattttggat ttgaatcaa 5100
113 gcaatatgga agcaaccagc aaattaacta atttaagtac atttttaaaa aaagagctaa 5160
114 gataaagact gtggaaatgc caaaccaagc aaatttagaa ccttgcaacg gtatccaggg 5220
115 actatgatga gaggccagca cattatcttc atatgtcacc tttgctacgc aaggaaattt 5280
116 gtcagttcg tatacttcgt aagaaggaat gcgagtaagg attggcttga attccatgga 5340
117 atttcttagta tgagactatt tatatgaagt agaaggtaac tcttgacaca taaattggta 5400
118 taataaaaag aaaaacacaa acattcaaag cttagggata ggtccttggg tcaaaagttg 5460
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122 <211> LENGTH: 1308
123 <212> TYPE: PRT
124 <213> ORGANISM: Homo sapiens
126 <400> SEQUENCE: 2
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128 1 5 10 15
129 Ala Gly Thr Val Gln Pro Ser Asp Ser Gln Ser Val Cys Ala Gly Thr
130 20 25 30
131 Glu Asn Lys Leu Ser Ser Leu Ser Asp Leu Glu Gln Gln Tyr Arg Ala
132 35 40 45
133 Leu Arg Lys Tyr Tyr Glu Asn Cys Glu Val Val Met Gly Asn Leu Glu
134 50 55 60
135 Ile Thr Ser Ile Glu His Asn Arg Asp Leu Ser Phe Leu Arg Ser Val
136 65 70 75 80
137 Arg Glu Val Thr Gly Tyr Val Leu Val Ala Leu Asn Gln Phe Arg Tyr
138 85 90 95
139 Leu Pro Leu Glu Asn Leu Arg Ile Ile Arg Gly Thr Lys Leu Tyr Glu
140 100 105 110
141 Asp Arg Tyr Ala Leu Ala Ile Phe Leu Asn Tyr Arg Lys Asp Gly Asn
142 115 120 125
143 Phe Gly Leu Gln Glu Leu Gly Leu Lys Asn Leu Thr Glu Ile Leu Asn
144 130 135 140
145 Gly Gly Val Tyr Val Asp Gln Asn Lys Phe Leu Cys Tyr Ala Asp Thr
146 145 150 155 160
147 Ile His Trp Gln Asp Ile Val Arg Asn Pro Trp Pro Ser Asn Leu Thr
148 165 170 175
149 Leu Val Ser Thr Asn Gly Ser Ser Gly Cys Gly Arg Cys His Lys Ser
150 180 185 190
151 Cys Thr Gly Arg Cys Trp Gly Pro Thr Glu Asn His Cys Gln Thr Leu
152 195 200 205
153 Thr Arg Thr Val Cys Ala Glu Gln Cys Asp Gly Arg Cys Tyr Gly Pro
154 210 215 220
155 Tyr Val Ser Asp Cys Cys His Arg Glu Cys Ala Gly Gly Cys Ser Gly
156 225 230 235 240
157 Pro Lys Asp Thr Asp Cys Phe Ala Cys Met Asn Phe Asn Asp Ser Gly

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158	245	250	255	
159	Ala Cys Val Thr Gln Cys Pro Gln Thr Phe Val Tyr Asn Pro Thr Thr			
160	260	265	270	
161	Phe Gln Leu Glu His Asn Phe Asn Ala Lys Tyr Thr Tyr Gly Ala Phe			
162	275	280	285	
163	Cys Val Lys Lys Cys Pro His Asn Phe Val Val Asp Ser Ser Ser Cys			
164	290	295	300	
165	Val Arg Ala Cys Pro Ser Ser Lys Met Glu Val Glu Glu Asn Gly Ile			
166	305	310	315	320
167	Lys Met Cys Lys Pro Cys Thr Asp Ile Cys Pro Lys Ala Cys Asp Gly			
168	325	330	335	
169	Ile Gly Thr Gly Ser Leu Met Ser Ala Gln Thr Val Asp Ser Ser Asn			
170	340	345	350	
171	Ile Asp Lys Phe Ile Asn Cys Thr Lys Ile Asn Gly Asn Leu Ile Phe			
172	355	360	365	
173	Leu Val Thr Gly Ile His Gly Asp Pro Tyr Asn Ala Ile Glu Ala Ile			
174	370	375	380	
175	Asp Pro Glu Lys Leu Asn Val Phe Arg Thr Val Arg Glu Ile Thr Gly			
176	385	390	395	400
177	Phe Leu Asn Ile Gln Ser Trp Pro Pro Asn Met Thr Asp Phe Ser Val			
178	405	410	415	
179	Phe Ser Asn Leu Val Thr Ile Gly Gly Arg Val Leu Tyr Ser Gly Leu			
180	420	425	430	
181	Ser Leu Leu Ile Leu Lys Gln Gln Gly Ile Thr Ser Leu Gln Phe Gln			
182	435	440	445	
183	Ser Leu Lys Glu Ile Ser Ala Gly Asn Ile Tyr Ile Thr Asp Asn Ser			
184	450	455	460	
185	Asn Leu Cys Tyr Tyr His Thr Ile Asn Trp Thr Thr Leu Phe Ser Thr			
186	465	470	475	480
187	Ile Asn Gln Arg Ile Val Ile Arg Asp Asn Arg Lys Ala Glu Asn Cys			
188	485	490	495	
189	Thr Ala Glu Gly Met Val Cys Asn His Leu Cys Ser Ser Asp Gly Cys			
190	500	505	510	
191	Trp Gly Pro Gly Pro Asp Gln Cys Leu Ser Cys Arg Arg Phe Ser Arg			
192	515	520	525	
193	Gly Arg Ile Cys Ile Glu Ser Cys Asn Leu Tyr Asp Gly Glu Phe Arg			
194	530	535	540	
195	Glu Phe Glu Asn Gly Ser Ile Cys Val Glu Cys Asp Pro Gln Cys Glu			
196	545	550	555	560
197	Lys Met Glu Asp Gly Leu Leu Thr Cys His Gly Pro Gly Pro Asp Asn			
198	565	570	575	
199	Cys Thr Lys Cys Ser His Phe Lys Asp Gly Pro Asn Cys Val Glu Lys			
200	580	585	590	
201	Cys Pro Asp Gly Leu Gln Gly Ala Asn Ser Phe Ile Phe Lys Tyr Ala			
202	595	600	605	
203	Asp Pro Asp Arg Glu Cys His Pro Cys His Pro Asn Cys Thr Gln Gly			
204	610	615	620	
205	Cys Asn Gly Pro Thr Ser His Asp Cys Ile Tyr Tyr Pro Trp Thr Gly			
206	625	630	635	640

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207 His Ser Thr Leu Pro Gln His Ala Arg Thr Pro Leu Ile Ala Ala Gly
208 645 650 655
209 Val Ile Gly Gly Leu Phe Ile Leu Val Ile Val Gly Leu Thr Phe Ala
210 660 665 670
211 Val Tyr Val Arg Arg Lys Ser Ile Lys Lys Lys Arg Ala Leu Arg Arg
212 675 680 685
213 Phe Leu Glu Thr Glu Leu Val Glu Pro Leu Thr Pro Ser Gly Thr Ala
214 690 695 700
215 Pro Asn Gln Ala Gln Leu Arg Ile Leu Lys Glu Thr Glu Leu Lys Arg
216 705 710 715 720
217 Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys Gly Ile
218 725 730 735
219 Trp Val Pro Glu Gly Glu Thr Val Lys Ile Pro Val Ala Ile Lys Ile
220 740 745 750
221 Leu Asn Glu Thr Thr Gly Pro Lys Ala Asn Val Glu Phe Met Asp Glu
222 755 760 765
223 Ala Leu Ile Met Ala Ser Met Asp His Pro His Leu Val Arg Leu Leu
224 770 775 780
225 Gly Val Cys Leu Ser Pro Thr Ile Gln Leu Val Thr Gln Leu Met Pro
226 785 790 795 800
227 His Gly Cys Leu Leu Glu Tyr Val His Glu His Lys Asp Asn Ile Gly
228 805 810 815
229 Ser Gln Leu Leu Asn Trp Cys Val Gln Ile Ala Lys Gly Met Met
230 820 825 830
231 Tyr Leu Glu Glu Arg Arg Leu Val His Arg Asp Leu Ala Ala Arg Asn
232 835 840 845
233 Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr Asp Phe Gly Leu
234 850 855 860
235 Ala Arg Leu Leu Glu Gly Asp Glu Lys Glu Tyr Asn Ala Asp Gly Gly
236 865 870 875 880
237 Lys Met Pro Ile Lys Trp Met Ala Leu Glu Cys Ile His Tyr Arg Lys
238 885 890 895
239 Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Ile Trp Glu
240 900 905 910
241 Leu Met Thr Phe Gly Gly Lys Pro Tyr Asp Gly Ile Pro Thr Arg Glu
242 915 920 925
243 Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile
244 930 935 940
245 Cys Thr Ile Asp Val Tyr Met Val Met Val Lys Cys Trp Met Ile Asp
246 945 950 955 960
247 Ala Asp Ser Arg Pro Lys Phe Lys Glu Leu Ala Ala Glu Phe Ser Arg
248 965 970 975
249 Met Ala Arg Asp Pro Gln Arg Tyr Leu Val Ile Gln Gly Asp Asp Arg
250 980 985 990
251 Met Lys Leu Pro Ser Pro Asn Asp Ser Lys Phe Phe Gln Asn Leu Leu
252 995 1000 1005
253 Asp Glu Glu Asp Leu Glu Asp Met Met Asp Ala Glu Glu Tyr Leu Val
254 1010 1015 1020
255 Pro Gln Ala Phe Asn Ile Pro Pro Pro Ile Tyr Thr Ser Arg Ala Arg

VERIFICATION SUMMARY

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Output Set: N:\CRF3\09182001\I940101.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date